IN THE SPECIFICATION:

Please replace paragraph at page 18, line 12 through page 19, line 4, with the following amended paragraph:

The probe 1 at final concentration of 0.25 μM is hybridized (annealed at 55°C for 1 min) to the genome, which has been previously ~~degenerated~~ denatured at 95°C for 30 sec, and the first synthesis of complementary strands is carried out at 72°C. for 3 min. The complementary strand regions elongated in this first synthesis are shown by 5-1, 5-2, . . . 5-n. Although various species of primers coexist, any of the byproducts that block the reaction is not produced because the reaction is not repeated as in the case of PCR. Excess of the primer 1 was removed by washing immediately after the synthesis of complementary strands. The primers elongated by the synthesis, 6-1, 6-2, . . . 6-n, are maintained with being hybridized to the genome 2-1 and 2-2. The elongated primers, 6-1, 6-2, . . . 6-n, are then isolated from the genome by increasing the temperature of the solution up to 95-100°Cand collected. A group of DNA fragments (complementary strand-1; 6-1, 6-2, . . . 6-n) of various sequences that contain the subject DNA regions and an anchor sequence at their 5' termini are thus obtained.

Please replace paragraph at page 19, line 20 through page 20, line 18, with the following amended paragraph:

After removing the primer 21, the primer 25 (final concentration, 0.2 μM) having the same sequence as that of the anchor sequence 3 of the primer 1 and the primer 26 (final concentration, 1 μM) having the same sequence as that of the anchor sequence 22 of the primer 21 are added to the solution containing the product of the complementary strand synthesis 24 to perform PCR amplification. The conditions of the PCR are as follows; the solution consists of 0.25 μM of MgCl.sub.2, .times.10 PCR buffer of the commercial kit and 0.0625 units/μL of Taq DNA polymerase. The cycle consisting of ~~degeneration~~ denaturation at 95°C for 30 sec, annealing at 55°C for 30 sec and elongation at 72°C for 1 min is repeated 35 times, and then the reaction mixture is incubated at 72°C for 5 min so that the elongation reaction of the product is completed. There is a possibility that the primers 1 and 21 competitively inhibit the PCR by the primers 25 and 26. To remove the primer 21 effectively and prevent the inhibition, biotin is conjugated to the 5' terminus of the primer 1, and the product of the complementary strand synthesis is collected by means of avidin-labeled magnetic beads. Otherwise, the primer 21 is not

necessarily removed if the concentrations of the primers 25 and 26 are higher than that of the primer 21. When performing the PCR using 10 μL of a sample under these conditions, several dozens fmol of single-strand DNA are obtained.

Please replace paragraph at page 21, lines 6-20, with the following amended paragraph:

The solution 29 containing the single-strand DNA sample 28 thus obtained is added to a reaction vessel shown in FIG. 3. Although only one reaction vessel is shown in FIG. 3, the vessel corresponds to a single well (6 mm in diameter) of a microtiter plate in actual experiments. In each well of the reaction vessel are smaller subcells, 31-1, 31-2, . . . 31-n, to each of which different species of DNA probes, 32-1, 32-2, . . . 32-n, are immobilized. As shown in FIG. 4, a DNA oligomer containing the primer sequence 32 whose 3' terminus has been designed to hybridize to a mutation site N34 of the sample DNA 28 is immobilized to each subcell 31. Shortly, multiple subcells are set in each of the wells on a microtiter plate, and different probes are separately immobilized to each subcell.

Please replace paragraph at page 21, lines 6-20, with the following amended paragraph:

In example 1, the anchor primers are used for initiation of the synthesis of complementary strands without recognizing mutations in the targets. In example 2, primers that can recognize mutations are used in the first or the second synthesis of complementary strands in example 1. FIG. 9 indicates the construction of the primers used in example 2 of the genetic test of the invention. The first primer 81, which consists of multiple primers corresponding to different targets, contains the sequence 82 that is complementary to the target and the universal sequence 83 that is not hybridized with the target. The primer 81 is designed so that the 3' terminus 84 is located exactly at the mutated point 86 during hybridization. The same number of the primer 81 as that of mutations is prepared.

Please replace paragraph at page 28, line 19 through page 29, line 4, with the following amended paragraph:

Two primers, each of which corresponds to a wild type and a mutant, are prepared for each of the test sites for normal SNPs. These primers possess the universal sequence (anchor sequence 83) that is not hybridized with the target. The anchor sequence 83 is used as a priming region for amplification of DNA fragments by PCR or other methods in later steps. In addition,

the sequence ~~that recognizes~~ 87 to recognize mutations is introduced between the universal sequence 83 and the target-specific sequence 82 to detect mutations. FIGS. 10 and 11 show the construction of the primer 81 and the reaction steps including synthesis of complementary strands.

Please replace paragraph at page 30, line 27 through page 31, line 12, with the following amended paragraph:

The primer 98 with the sequence identical to the anchor sequence 83 and the primer 99 with that identical to the anchor sequence 96 are used for PCR amplification. The PCR product 315 (including the DNA strands 315-1 and 315-2) thus obtained is ~~degenerated~~ denatured to make the single-strand DNA 315-2, which is subsequently added to the reaction vessel to hybridize with the probe 32 in the subcell 61. By adding dNTPs (dATPαS, dGTP, dCTP, dTTP), the synthesis of complementary strands 106 is performed. Pyrophosphate PPi 107 produced in this reaction is converted to ATP, which is then reacted with luciferin to develop chemiluminescence. The following steps are the same as in example 1.

Please replace paragraph at page 32, lines 20-28, with the following amended paragraph:

The DNA strand 105 is ~~degenerated~~ denatured to produce the single-strand DNA 105-2, which is hybridized with the primer 32 immobilized to either the subcell 61 of the reaction vessel or the beads placed in the subcells to synthesize the complementary strand 111. Excess of the DNA strand 105-2 is removed by washing. With these procedures, different DNA strands are separately bound to each subcell; in some subcells, no synthesis of complementary strands occurs.

Please replace paragraph at page 43, lines 14-24, with the following amended paragraph:

FIG. 18 is an example, in which the 3' terminus 506 of the anchor probe 502 corresponds to the mutation site M (507) in the target. If the terminal sequence is not completely complementary to the target sequence, the ligation reaction does not occur. This means that the presence or absence of mutations could be determined by whether the ligation reaction occurs or not. After the ligation reaction, excess of the probes 501 and 502 is washed away, and double

strands are ~~degenerated~~ denatured to single strands to obtain the DNA fragment 510 produced in the ligation reaction.